

This Page Is Inserted by IFW Operations
and is not a part of the Official Record

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

- BLACK BORDERS
- TEXT CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

IMAGES ARE BEST AVAILABLE COPY.

**As rescanning documents *will not* correct images,
please do not report the images to the
Image Problem Mailbox.**

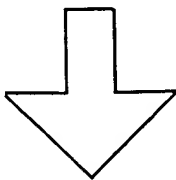
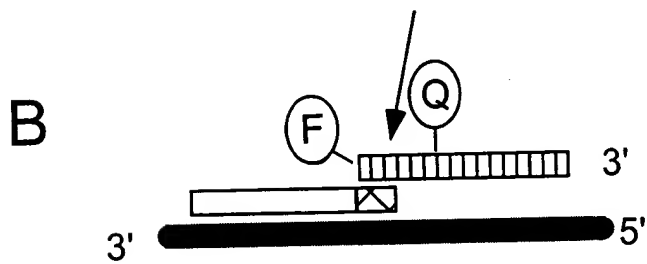
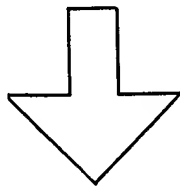
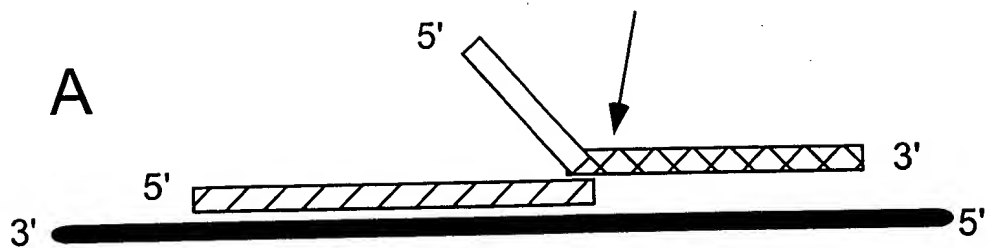


FIGURE 1

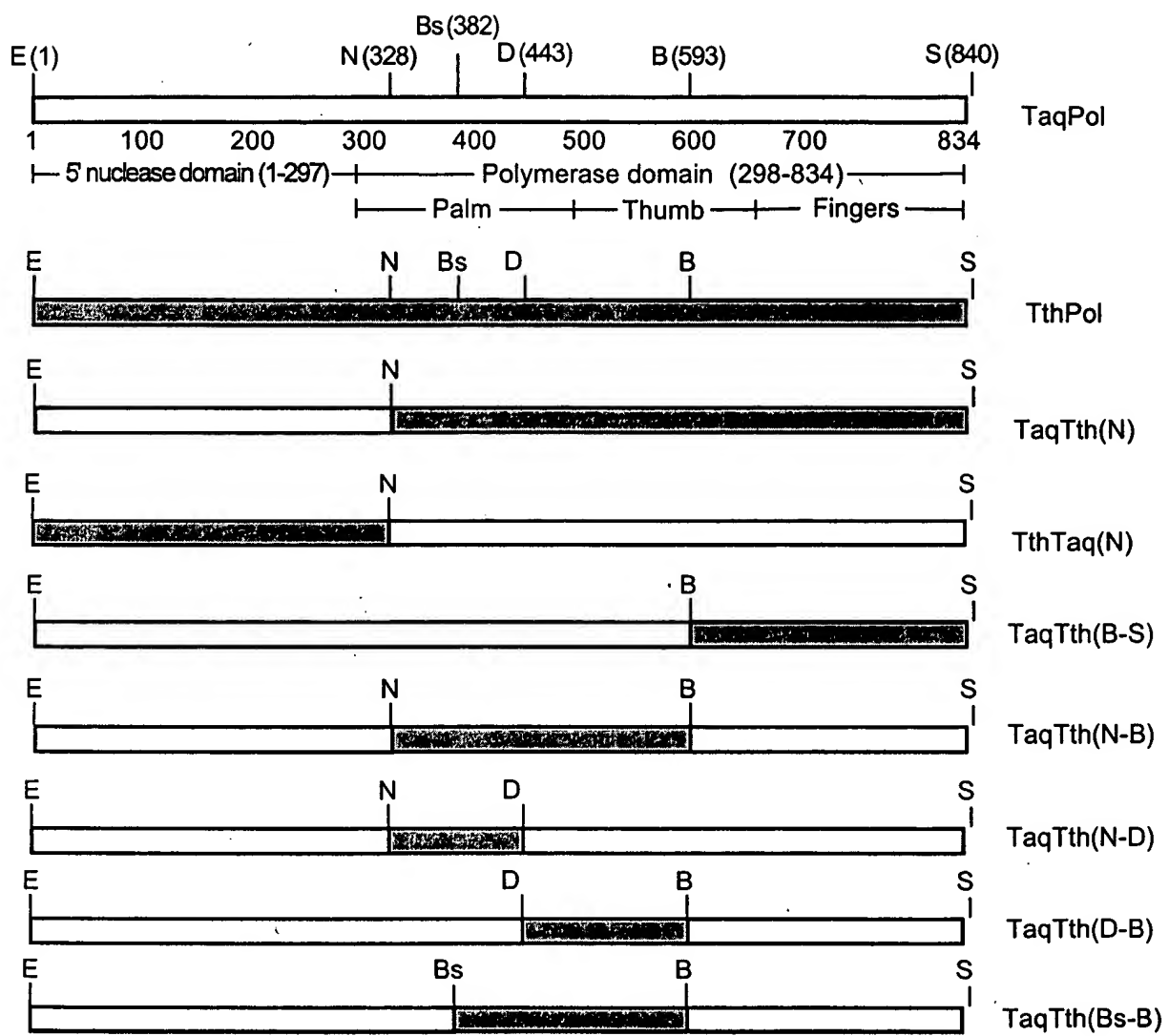


FIGURE 7



MAJORITY	[SEQ ID NO:7]	CGAGCGGAGGACGTXCTGGCCACCCCTGGCCCAAGAGCCGGAAAGGAGGGGTACGAGGTGGCGCATCCTC	417
DNAPTAA	[SEQ ID NO:1]C.....G.....C.....C.....	417
DNAPTFL	[SEQ ID NO:2]	T.....G.....CG.....	414
DNAPTTH	[SEQ ID NO:3]T.C.....	420
MAJORITY		ACGCGCGACCGCGGACCTCTACGAGCTCCTTCCGACCGCATCGCCGTCCTCCACCGCGAGGGGTACCTCA	
DNAPTAA	AAA.....T.....CA.....	487
DNAPTFL		T.....G.....G.G.....A.....T.....G.	484
DNAPTTH	A.G.C.....G.....CC.....	490
MAJORITY		TACCGCGCGCGGTGGCTTGGGAGAAGTACGGCCTGAGGCGGAGCAGTGGGTGGACTACCGGGCGCCTGGC	
DNAPTAA	C.....A.....C.....C.....CC.....A.	557
DNAPTFL	AC.....C.C.....	554
DNAPTTH	A.....C.....T.C.....C.T	560
MAJORITY		GGGGGACCCCTCGGACAACCTCCCGCGGCTCAAGGGCATCGGGGAGAGACCGCCXGAAGCTCCTCXAG	
DNAPTAA		C.....GAG.....T.....G.GAG.....T..GG..	627
DNAPTFL	G.T.A.....G.....A.G....A..CGC	624
DNAPTTH	TC.....A..	630
MAJORITY		GAGTGGGGGAGCCCTGGAAAAACCTCCTCAAGAACCTGGACCGGCTGAAGCCGCC -- CXTCGGGGGAGAAGA	
DNAPTAA	GC.....C.....A.....	694
DNAPTFL	T.C.C.....A.....T..T.G.....C	691
DNAPTTH	A.....A.....A.AAAA.G.....	700

FIG. 8C

MAJORITY [SEQ ID NO:7] TCCAGGCCACATGGAXGACCTGAXGCTCTCCTGGGAGGCTXGCCAGGTGGGACGGACCTGCCCGCTGGA
DNAPTAO [SEQ ID NO:1] ...T...C...T...A...C...GG...A... 764
DNAPTFL [SEQ ID NO:2] ...GGG...G...C...GCC...T...C...A...T...A...T... 761
DNAPTTH [SEQ ID NO:3] ...A...C...A...C...G...T...C...G...C... 770

MAJORITY GGTGGACTTCGGCAAGXGGCGGAGCGCGGAGCGGGGCTTAGGGGCTTCTGGAGAGGCTGGAGTTT
DNAPTAO ...AA... 834
DNAPTFL ...GG.G.C.C.CACA...A...T...T...GG...T...T...C...T... 831
DNAPTTH ...C...C...G... 840

MAJORITY GGCAGCCTCCTCCAGGAGTTCGGGCTTCGTGGAGGGGGCCCAAGGCCCTGGAGGAGGCCCGCTGGCCCCGGC
DNAPTAO ...T...AA... 904
DNAPTFL ...A...G...G...G...GGA...T... 901
DNAPTTH ...G...G...G... 910

MAJORITY CCGAAGGGGCTTCGTGGGCTTGTGCTTTCGGGCGCGGAGGCCCATGTGGGCGGAGCTTCTGGCCCCTGGC
DNAPTAO ...G...AAG...T... 974
DNAPTFL ...T...T...TC.T...T... 971
DNAPTTH ...C...C...G...AAA... 980

MAJORITY CCGCGCGCAGGGAGGGCGGGTCCACCGGGGACGACAGACCCCTTTAXCGGCGCTXAGCGACCTXAAGCAGCTG
DNAPTAO ...G... 1044
DNAPTFL ...T.GG...GT...G...CC...T...A...C...T.A...AA.C...C...G...C... 1041
DNAPTTH ...TG...C...G...G...G...G...G...G...G...A.A...C...C...C... 1050



FIG. 8D

MAJORITY [SEQ ID NO:7]		CGGGGXTCTCTGGCCAAGGACCTGGCCGTTTGGCCCTGAGGGAGGGCCCTXGACCTCTGCCCGGGGACG	
DNAPTAA	[SEQ ID NO:1]G..T.....A.....AG.....C.....A.....T.G.....CC.....C.....	1114
DNAPTFL	[SEQ ID NO:2]AA.....G.....G.....C.....C.....T.C..A.A.....	1111
DNAPTTH	[SEQ ID NO:3]C.....C.....C.....TC.....G..A.....G.....	1120
MAJORITY		ACCCCATGCTCTCTGGCTACCTCCTGGACCCCTCCAAGACCACCCCGAGGGGTGGCCCGGGCTACGG	
DNAPTAA	T.....	1184
DNAPTFL	G.....T.....T.....	1181
DNAPTTH	G.....G.....	1190
MAJORITY		GGGGGAGTGGACGGGAGXCGGGGGAGCGGGCCCTCCTXTCCGAGAGGCTCTCCXGAACCTXXGGAG	
DNAPTAA	G.....G.....T.....GCC.....GTG..G..	1254
DNAPTFL	T.....A.....GG.....C.C.....A..C...AAA.....	1251
DNAPTTH	C..C.CCC.C.....C..G.....CAT.G.....CCTTA..	1260
MAJORITY		CGCCTTGAGGGGAGGAGGCTCCTTTGGCTTTACGAGGAGGTGGAGAACCCCTTCCCGGGTGGTGG	
DNAPTAA		A..G.....G.....G.....G.....GCT.....	1324
DNAPTFL	A...A..A..C.C..G.....G.....G.....GT.....	1321
DNAPTTH	C.....A.....C.....C.....A.....G.....	1330
MAJORITY		CCACATGGAGGCCACGGGGGTXCGGCTGGACGTGGCCTACCTCCAGGCCCTXGCTGGAGGTGGCGGA	
DNAPTAA	G..C.....T...AG.....T.G.....C...	1394
DNAPTFL	GG.....C.....C.....C.....A..C	1391
DNAPTTH	C.....A.....T.....T.....C.T.....	1400

FIG. 8E

MAJORITY [SEQ ID NO:7] GGAGATCGCGCGCGCTCGAGCAGGAGGTCTTCGGCCTGGCGCGCCACCCCTTCAACCTCAACTCCCCGGGAC

DNAPTAQ [SEQ ID NO:1]CC.....CC..... 1464

DNAPTFL [SEQ ID NO:2]G.G....AG..G.....C.....C... 1461

DNAPTTH [SEQ ID NO:3]T.....T...G..... 1470

MAJORITY CAGCTGGAAGGGTGCTCTTGACGAGCTXGGGCTTCCCGCCATCGGCAAGACGGAGAGACXGGCAAGC

DNAPTAQC.....A.....C..... 1534

DNAPTFLGC.....G..C..G..T.....G..G..A. 1531

DNAPTTHTA.....T.G..G.....C.A..... 1540

MAJORITY GCTCCACGAGCGCGCGCTGCTGGAGGGCCTXCGXGAGCGCCACCCCATCGTGGAGAAGATCCTGCAGTA

DNAPTAQC.....C..C..... 1604

DNAPTFLT.....G..A.....CGC..... 1601

DNAPTTHG.....A..G.....C...C. 1610

MAJORITY CCGGAGGCTCACCAAGCTCAAGAACACCTACATXGACCGCCTGCCXGXCCTCGTGCACCCCGAGCGGGC

DNAPTAQG....G.....T....T....G.A....A..... 1674

DNAPTFLA.....A.....C.C...G.....A...C... 1671

DNAPTTHG.G.....G.G.....C..AAG.....G..... 1680

MAJORITY CGCCTCCACACCGCGCTTCAACCAGACGGGCCACGGCCAGCGGCGGCTTAGTAGCTCGGAGCCCAAGCTGC

DNAPTAQA.....T.....C. 1744

DNAPTFLG.....C.....TCC..... 1741

DNAPTTHG..... 1750



FIG. 8F

MAJORITY	ESEQ ID NO:71	AGAACATCGCGGCTCGGCAGCCGCTGGGCCAGAGGATCGCGCGGGCCCTTCGTGCCCGAGGAGCGGXTGGGT	
DNAPTAQ	[SEQ ID NO:1]G..T..G.....A..C.....G...C..	1814
DNAPTFL	[SEQ ID NO:2]G.....T.....C..C.....A.....C.....	1811
DNAPTTH	[SEQ ID NO:3]CT.....C.....C.....C.....T.....C..	1820
MAJORITY		GTGGTGGCCCTGGAGTATAGCCAGATAGAGCTCGGGGTCTCGGCCACCTCTCGGGGAGCGAGAACCTG	
DNAPTAQ		A.....T.....C.....A.....G.....C.....	1884
DNAPTFL	T..T.....C.....T.....T.....C.....	1881
DNAPTTH	T.....C.....C.....C.....A.....	1890
MAJORITY		ATCGGGGTCTTCAGGAGGGGAGGACATCCACACCCAGACCGCCAGCTGGATGTTGGGGCTCCCCCGGG	
DNAPTAQ	C.....C.....GG.....G.....G..	1954
DNAPTFL	T.....T.....T.....TT....C..	1951
DNAPTTH	A.....A.....A.....A.....	1960
MAJORITY		AGGCGGTGGACCCCTGATCGCGCGGGGGCCCAAGACCATCAACTTCGGGGTCCTCTACGGGCATGTCCGC	
DNAPTAQ	A..G..A.....T.....G.....G..	2024
DNAPTFL	G.....G.....G.....G.....	2021
DNAPTTH	GG..G.....C.....C.....	2030
MAJORITY		CCACCGCCTCTCCAGGAGCTTCCCATCCCCTACGAGGAGGGGTGGCCCTTCATTGACGGCTACTCCAG	
DNAPTAQ	A.....T.....CCA.....T...	2094
DNAPTFL	GG.....T.....T.....	2091
DNAPTTH		...TA.G.....T.....T..A.....A..	2100



FIG. 8G

MAJORITY [SEQ ID NO:7]	AGCTTCCCCAAGGTGGGGCCCTGGATTGAGAAGAGCCCTGGAGGAGGGCCAGGAGGGGGGTACGTGGAGA	
DNAPTAO [SEQ ID NO:1]	2164
DNAPTFL [SEQ ID NO:2]	...A.....GG.....C.....C.CC.....T.....	2161
DNAPTTH [SEQ ID NO:3]A.A.....G.....A.....C.....A.	2170
MAJORITY	CCCTCTTGGGGCCGGCCCTACGTGCCCGACCTCAACGGCGGGGTGAAGAGCGTGGGGGAGGGGGCGGA	
DNAPTAOC.....A.....AG.G.....C.....	2234
DNAPTFLT.....C.....	2231
DNAPTTH	...AA.AA.....GA.....C.....	2240
MAJORITY	GGCATGGCCCTTCAACATGCCCGTCCAGGGCAGCGGGCCGACCTCATGAAGCTGGCCATGGTGAAGCTC	
DNAPTAO	2304
DNAPTFLG.....T.....CG...T	2301
DNAPTTHC.....	2310
MAJORITY	TTCCCGGGCTXCAGGAAATGGGGCCAGGATGCTCCTXCAGGTCACAGGAGGCTGCTCCTGGAGGGCC	
DNAPTAOA...GG.....T.....	2374
DNAPTFLT...C.....G.....TT.G.....G.....	2371
DNAPTTHC.C.G...G.....C.C.....C.....CC.....G.....	2380
MAJORITY	CCAAAGAGCGGGGGAGGXGGTGGCCGGCTTGGCCCAAGGAGGTCATGCAGGGGGGTCTATCCCCCTGGCCGT	
DNAPTAOA.....CC.....GGCC.....G.....	2444
DNAPTFLG.C.....AG...A.....CC.....CAG...	2441
DNAPTTHC...C.....C...A.....G.....C.....AA.C.....C.....	2450

FIG. 8H

MAJORITY [SEQ ID NO:7] GCGCGCTGGAGGCTGGGGCATGGGGGAGGAGCTGGCTCTCCGCCCAAGGAGTAG

DNAPTAA [SEQ ID NO:1]

DNAPTFL [SEQ ID NO:2]

DNAPTTH [SEQ ID NO:3]

.....A.....GA
.....CC.....
.....T.....GT...

2499

2496

2505





FIG. 9A

MAJORITY [SEO ID NO:8] MXAML PLFEPKGRVLLVDGHHLAYRTFFALKGLTTSRGEVPQAVYGFAKSLKALKEDG- DAVXVVFDAK

TAO PRO [SEO ID NO:4] .RG.....H.....I..... 69
TFL PRO [SEO ID NO:5]V.V..... 68
TTH PRO [SEO ID NO:6] .E.....YK..F..... 70

MAJORITY APSFRHEAYEAYKAGRPTPEDFPROLALI KELVDLLGLXRLEVPGEADDVLATLAKKAEKEGYEVRI L

TAO PROGG.....A.....S..... 139
TFL PROV.....F.....R..... 138
TTH PROFT..... 140

MAJORITY TADRDLYOLLSDRI AVLHPEGYLI TPWLWEKYGLRPEQWVDYRALXGDPSPDNLPGVKGI GEKTAXKLLX

TAO PROK.....H.....D..A...T..E.....R...E 209
TFL PROE..I.....Y.....A.....I.....QR..I R 208
TTH PROV...V.....H...E.....F...V.....L...K 210

MAJORITY EWGSLENLLKNLDRVKP- XXREKI XAHMEDLXLSXXLSXVRTDLPLEVDFAXRREPDRGLRAFLELRF

TAO PROA.....L...AI...L...D..K..WD.AK.....K.....R..... 278
TFL PROFOH..O...SL...LQ.G..A.A..RK..O.H.....GR..T.NL..... 277
TTH PROENV.....K..L...R..LE..R.....L.OG..... 280

MAJORITY GSLLHEFGLLEXPKALEEAPWPPPEGAFVGFVLSRPEPMWAEILLALAAARXGRVHRAXDPLXGLRDLKEV

TAO PROS.....K.....D.....G.....PE.YKA.....A 348
TFL PROG...A.....L..SF.....G.WE..L...O...R.....G. 347
TTH PROA.AP.....K.....C.D.....A..A..K..... 350



FIG. 9B

MAJORITY [SEQ ID NO: 8] RGLLAKDLAVLALREGLDXPGDDPML LAYLLDPSNTTPEGVARRYGGWTE DAGERALLSERLFXNLXX

TAQ PRO [SEQ ID NO: 4] S G. P E A A WG 418
TFL PRO [SEQ ID NO: 5] I F. E A QT. KE 417
TTH PRO [SEQ ID NO: 6] S V AH HR. LK 420

MAJORITY RLEGEERLLWLXYXEVEKPLSRVLAHMEATGVRLDVAYLOALSLEVAEEI RRLEEEVFRLAGHPFNLSRD

TAQ PRO R. R. A. R. A. A. 488
TFL PRO K. E. R. EA. V. Q. 487
TTH PRO K. H. L. 490

MAJORITY QLERVLFDELGLPAIGKTEKTKRSTSAAVLEALREAHPI VEKILQYRELTKLKNYI DPLPXLVHPRTG

TAQ PRO S. D. I. 558
TFL PRO DR. A. K. 557
TTH PRO R. L. Q. H. V. S. 560

MAJORITY RLHTRFNQIATATGRLLSSSDPNLQNI PVRTPLGORI RRAFVAEEGWXLVALDYSQIELRVLAHLSGDENL

TAQ PRO I. L. 628
TFL PRO V. V. 627
TTH PRO A. A. 630

MAJORITY I RVFQEGRDI HTQTASWMF GVPPEAVDPL MRRAAKTI NFGVLYGMSAHLRSOELAI PYEEAVAFIERFYFO

TAQ PRO E. R. O. 698
TFL PRO S. G. G. S. 697
TTH PRO K. V. 700

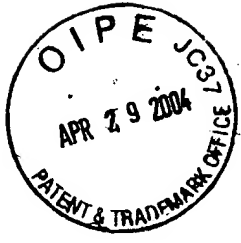


FIG. 9C

MAJORITY [SEQ ID NO:8] SFPKVRWIEKTL E E G R R R G Y V E T L F C R R R Y V P D L N A R V K S V R E A A E R M A F N M P V O G T A A D L M K L A M V K L

TAO PRO [SEQ ID NO:4] E 768
TFL PRO [SEQ ID NO:5] Y G R. 767
TTH PRO [SEQ ID NO:6] K 770

MAJORITY F P R L X E M G A R M L O V H D E L V L E A P K X R A E X V A A L A K E V M E G V Y P L A V P L E V E V G X G E D W L S A K E X

TAO PRO E A R I 833
TFL PRO O. L D R W. O L 831
TTH PRO R L O A E A K A M G 835

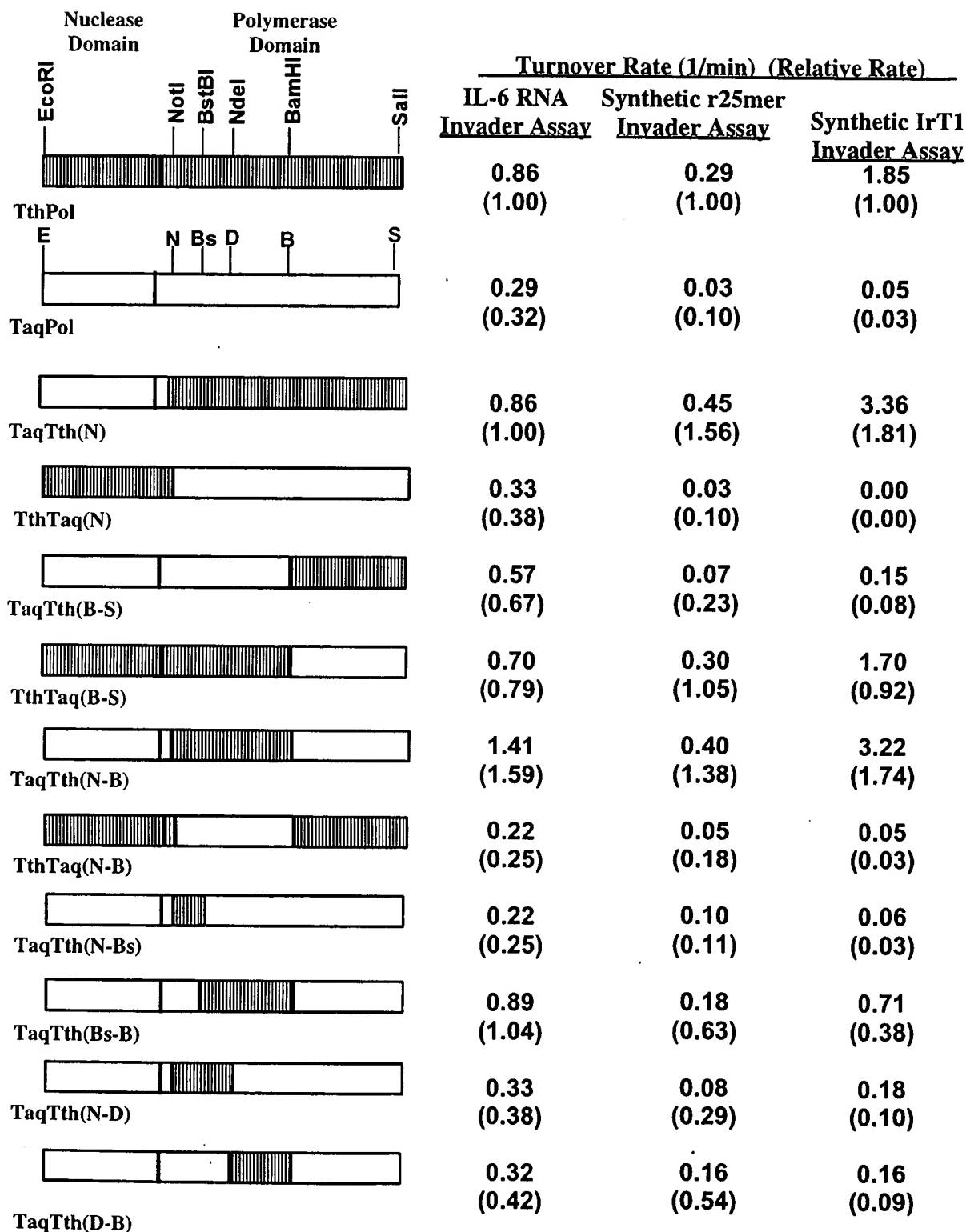


FIGURE 19

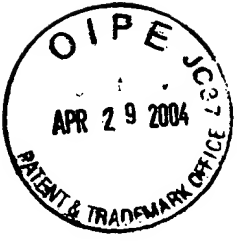


FIGURE 25

